

FIG. 1

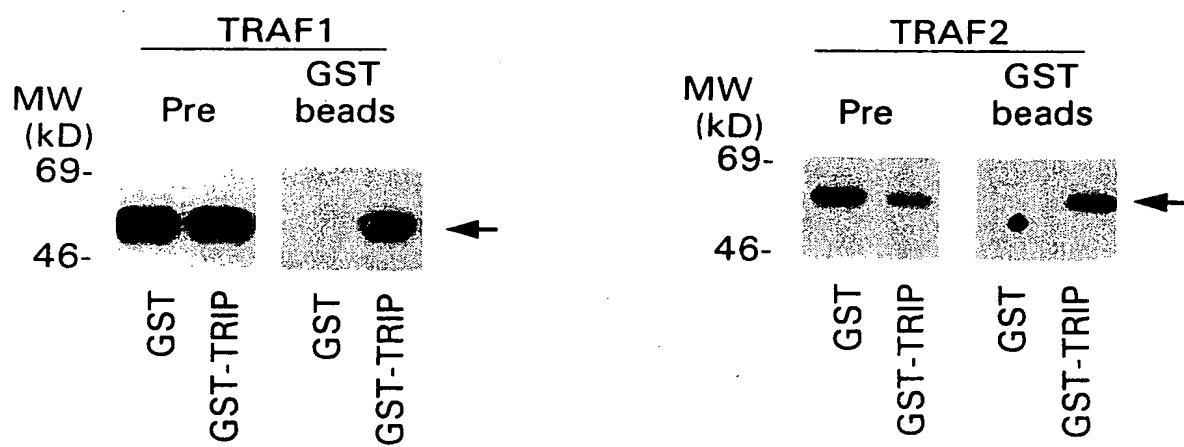


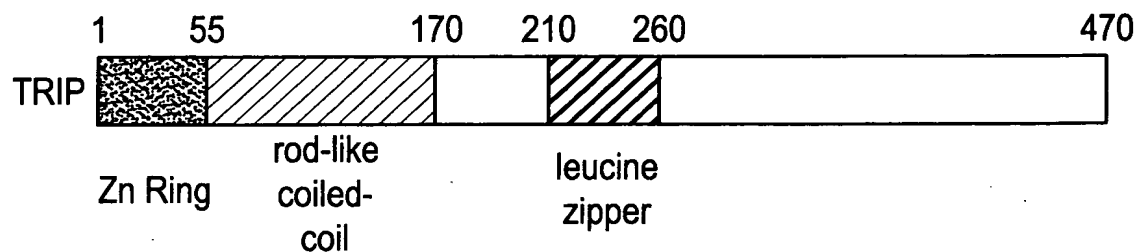
FIG. 2A-1

|     |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |       |       |
|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-------|-------|
| 1   | M | P | I | L | S | L | C | T | I | C | S | D | F | F | D | H | S | R | D | V | A | A | I | H | C | G | H | T | F | H     | mTRIP |
| 1   | - | - | - | R | A | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | M | D | - | - | - | - | - | hTRIP |       |
| 31  | L | Q | C | L | I | Q | W | F | E | T | A | P | S | R | T | C | P | Q | C | R | I | Q | V | G | K | K | T | I | I | N     | mTRIP |
| 31  | - | - | - | - | - | - | S | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | R | - | - | - | - | hTRIP |       |
| 61  | K | L | F | F | D | L | A | Q | E | E | E | N | V | L | D | A | E | F | L | K | N | E | L | D | S | V | K | A | Q | I     | mTRIP |
| 61  | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | R | - | - | - | - | - | - | - | N | - | R | - | - | - | hTRIP |       |
| 91  | S | Q | K | D | R | E | K | R | D | S | Q | A | I | I | D | T | L | R | D | T | L | E | E | R | N | A | T | V | E | S     | mTRIP |
| 91  | - | - | - | - | K | - | - | - | - | - | V | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | V | -     | hTRIP |
| 121 | I | Q | N | A | I | N | K | A | E | M | L | C | S | T | I | K | K | Q | M | K | F | I | E | Q | R | Q | D | E | T | K     | mTRIP |
| 121 | - | - | Q | - | G | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | Y | - | - | Q | - | - | - | - | - | hTRIP |       |
| 151 | Q | A | R | E | E | A | H | R | L | K | C | K | M | K | T | M | E | Q | I | E | L | L | Q | S | Q | R | S | E | V | -     | mTRIP |
| 151 | - | - | Q | - | - | - | G | - | - | R | S | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | L | P | - | -     | hTRIP |
| 181 | E | E | M | I | R | D | M | G | V | G | Q | S | A | V | E | Q | L | A | V | Y | C | V | S | L | K | K | E | Y | E | N     | mTRIP |
| 181 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | hTRIP |       |
| 211 | L | K | E | A | R | K | A | T | G | E | L | A | D | R | L | K | K | D | L | V | S | S | R | S | K | L | K | T | L | N     | mTRIP |
| 211 | - | - | - | - | - | - | - | S | - | - | V | - | - | K | - | R | - | - | F | - | - | - | - | - | - | - | Q | - | V | Y     | hTRIP |
| 241 | T | E | L | D | Q | A | K | L | E | L | R | S | A | Q | K | D | L | Q | S | A | D | Q | E | I | T | S | L | R | K | K     | mTRIP |
| 241 | S | - | - | - | - | - | - | - | - | - | K | - | - | - | - | - | - | - | - | - | - | K | - | - | M | - | - | - | - | -     | hTRIP |
| 271 | S | D | D | P | P | G | N | L | E | P | A | S | A | T | N | E | T | V | S | R | L | V | F | E | S | P | A | P | V | E     | mTRIP |
| 271 | L | T | M | L | Q | E | T | - | N | L | P | P | V | A | S | - | - | - | D | - | - | - | - | - | - | - | - | - | - | -     | hTRIP |
| 301 | M | M | N | P | R | L | H | Q | R | P | F | G | D | E | I | D | L | N | T | T | F | D | V | N | T | P | P | T | Q | T     | mTRIP |
| 301 | V | - | - | L | K | - | - | - | - | S | - | R | - | D | - | - | - | - | A | - | - | - | - | D | - | - | - | A | R | P     | hTRIP |

‘

Q S  
C W

# FIG. 2B



# FIG. 2D

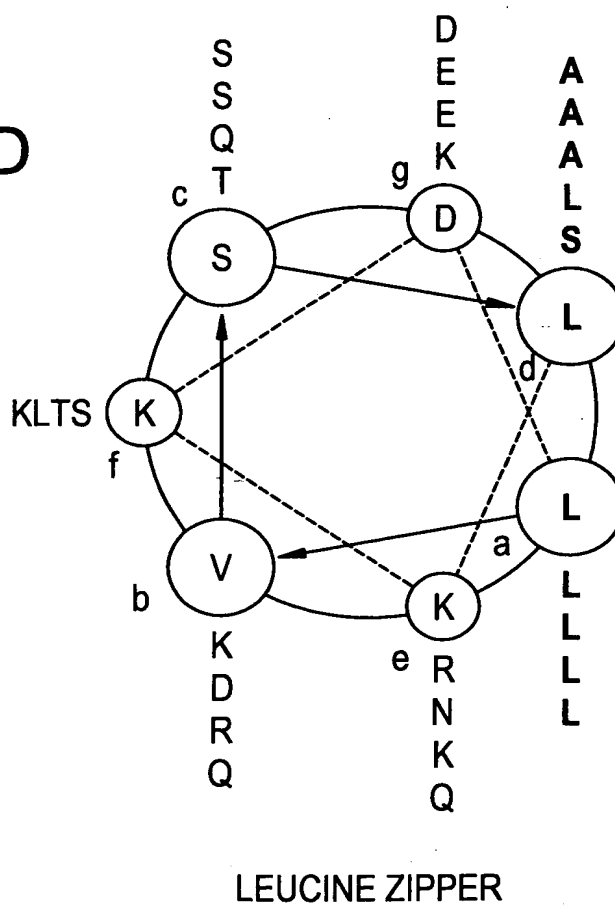
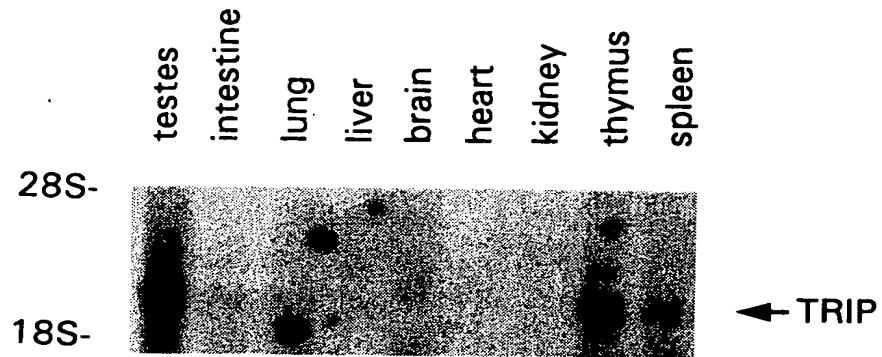


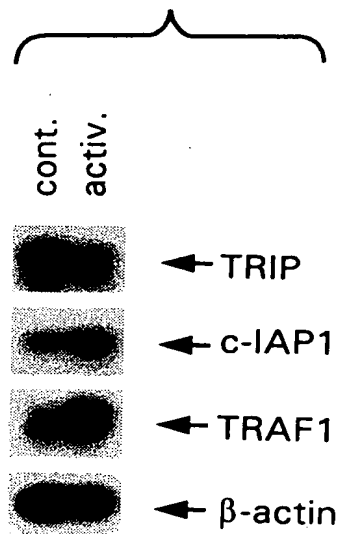
FIG. 2C

|           |     |   |
|-----------|-----|---|
| mTRIP     | 4   | LSLCTICSDFFDHSRDVAAIHCGHTF-HLQCLIQWFETAPSRTCPCQCR QVG |
| hTRIP     | 4   | RALCTICSDFFDHSRDVAAMDCGHTF-HLQCLIQSFETAPSRTCPCQCR QVG |
| mTRAF2    | 31  | KYLCACKN LRRPFQA---QCGHRY-CSFCLTS LSSGPQN-CAACVYEGL   |
| mTRAF3    | 48  | KYKCEKCR VLCNPKQT---ECGHRF-CESCMALLSSSSPK-CTACQ-ESI   |
| mc-IAP1   | 562 | ERTCKVCMDSREVS VFI---PCGHLVVCQECAPSLRK-----CPICGRGTI  |
| c-cbl     | 378 | FQLCKICAENDKDVK E---PCGHLM-CTSCLTSWQSEEGQG-CPFCRCEIK  |
| RING1     | 16  | ELMCPICLDMLKNTMTTK--ECLHRF-CSDC VTALRSGNKE-CPTCRKKLV  |
| SS-A/Ro   | 13  | EVTCPICLDPFVEPVSI---ECGHSF-CQEC SQVGKGGSV-CAVCRQRFL   |
| C-RZF     | 237 | YDVCA CLDEYEDGDKLR LPCSHAY-HCKCVDPWLT TKKT-CPVCKQKV   |
| neu       | 698 | SAECTICYENP DSVLY---MCGHMCNCYDCA EQWRGVGGGQCLCRAVIR   |
| consensus |     | ...C...C.....CGH...C...C.....C...C.....               |

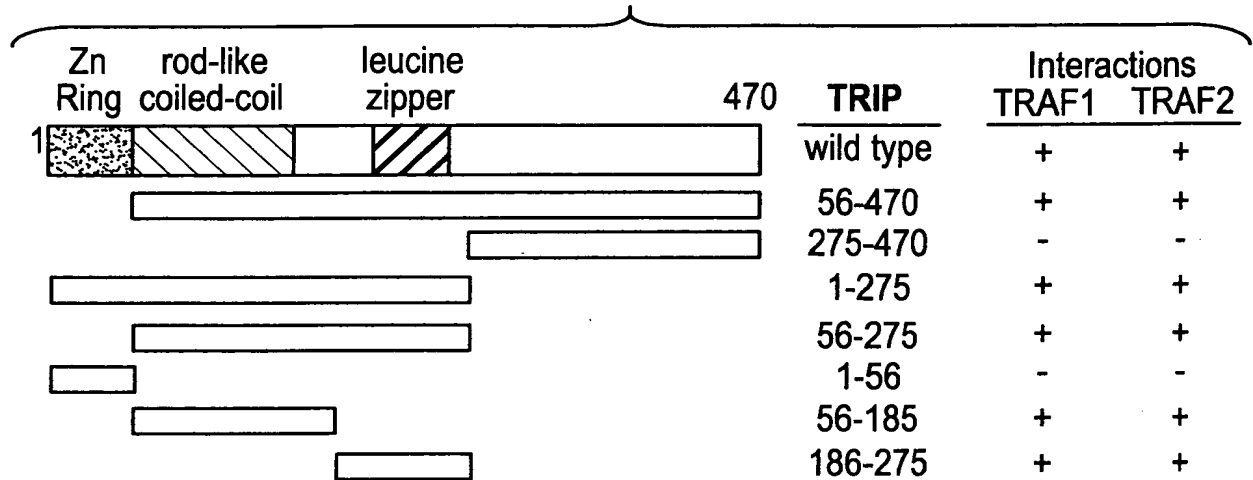
**FIG. 3A**



**FIG. 3B**



# FIG. 4A



# FIG. 4B

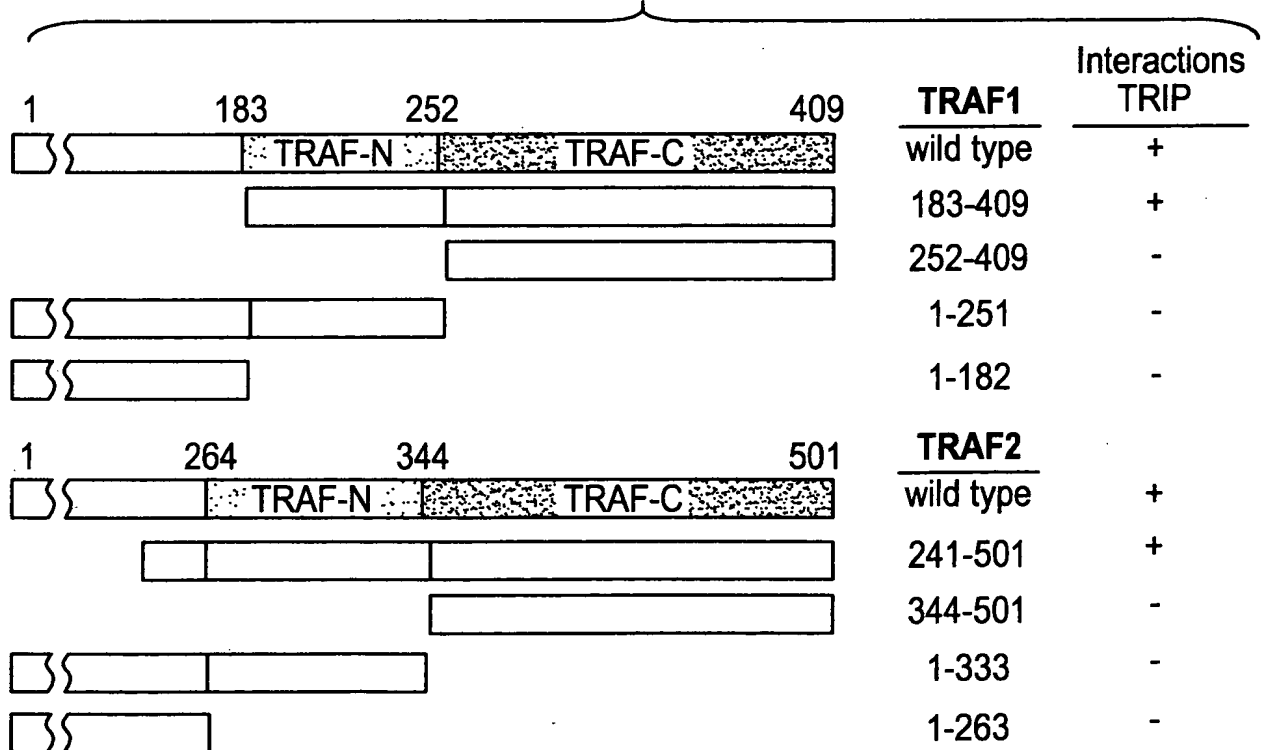


FIG. 5

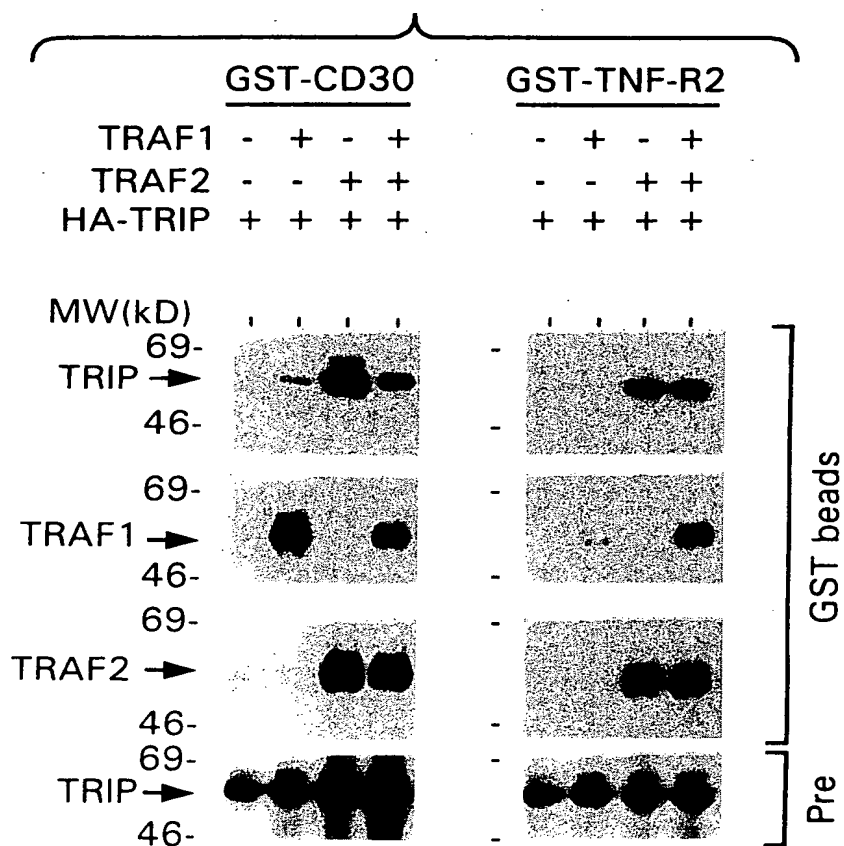




FIG. 6A

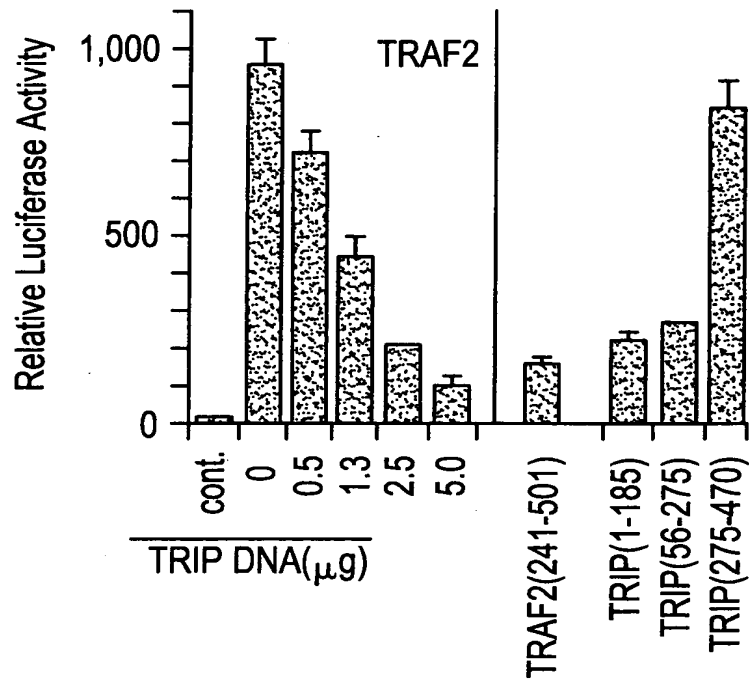


FIG. 6B

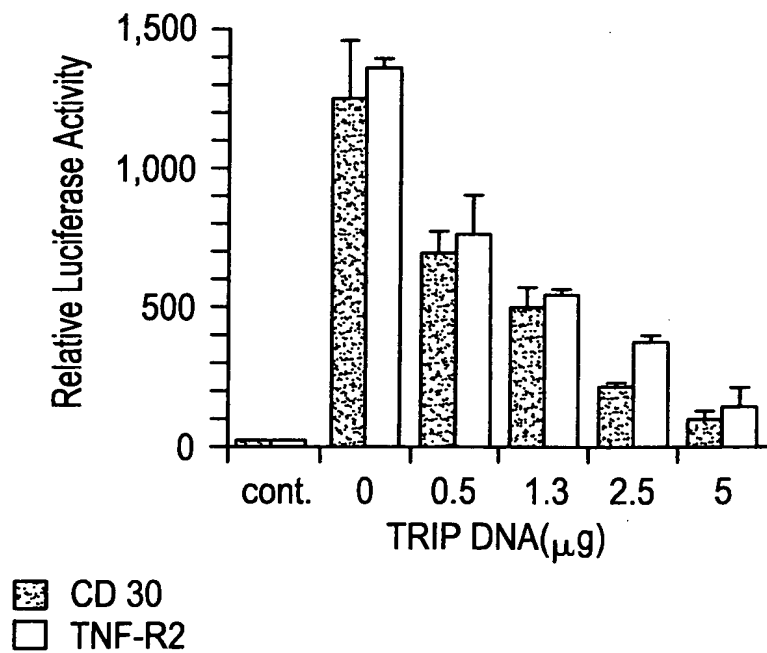


FIG. 6C

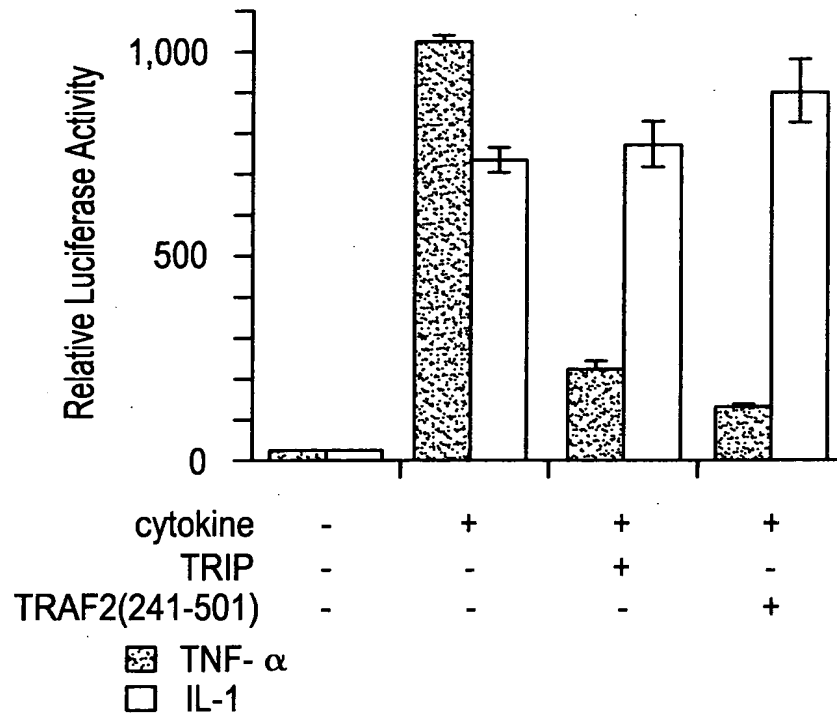


FIG. 6D

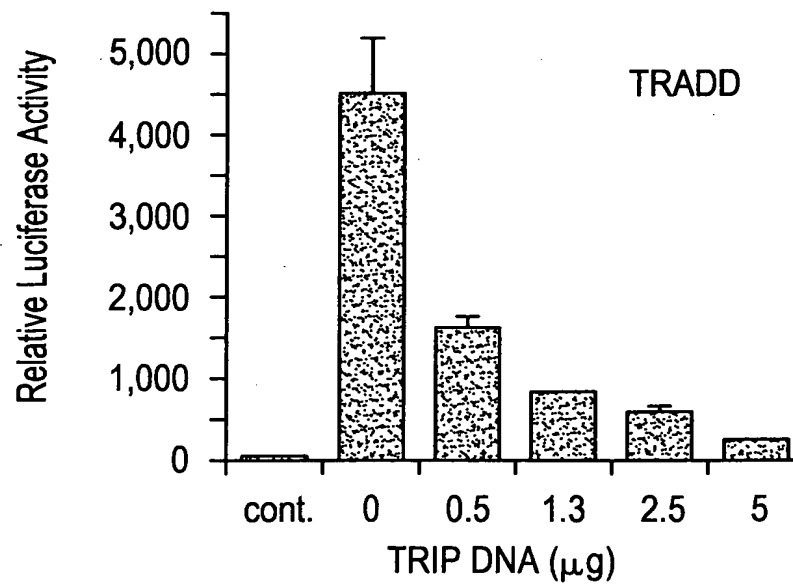
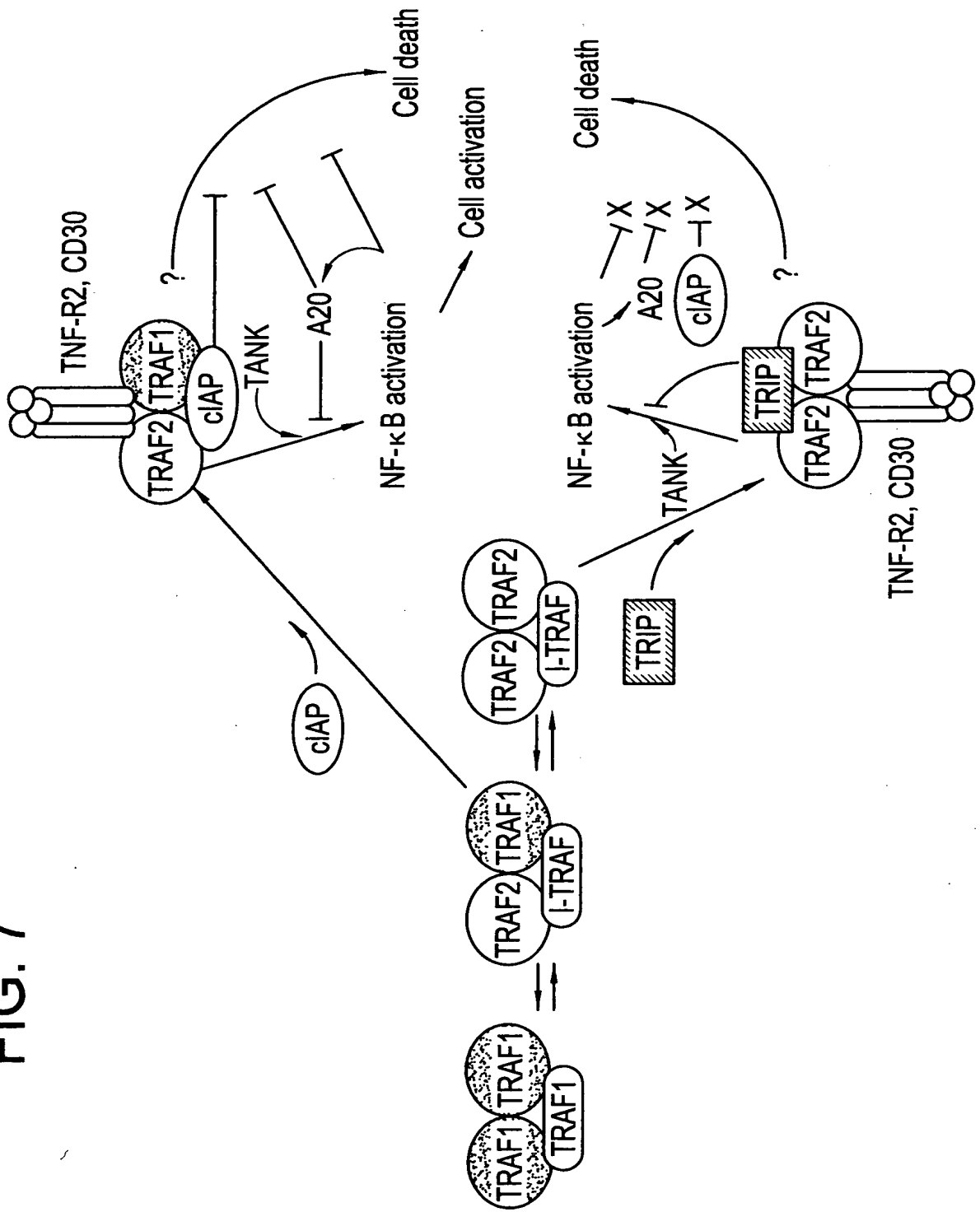


FIG. 7



## FIG. 8A

### Human TRIP cDNA sequence

GTGCGGTGGAGCGAAATTTGAAGCAAGCGGAGGCGGGGCGCTCTACGAAGCCGGAC  
CTGTAGCAGTTTCTTTGGCTGCCTGGGCCCCCTTGAGTCCAGCCATCATGCCTATCC  
GTGCTCTGTGCACTATCTGCTCCGACTTCTTCGATCACTCCCGCGACGTGGCCGCC  
ATCCACTGCGGCCACACCTTCCACTTGCAAGTGCCTAATTCAGTCCTTTGAGACAGC  
ACCAAGTCGGACCTGCCCACAGTGCCGAATCCAGGTTGGCAAAGAACCATTATCA  
ATAAGCTCTTCTTTGATCTTGCCCAGGAGGAGGAGAATGTCTTGGATCGAGAATTC  
TTAAGAATGAACTGGACAATGTCAGAGCCCAGCTTTCCCAGAAAGACAAGGAGAA  
ACGAGACAGCCAGGTCATCATCGACACTCTGCGGGATACGCTGGAAGAACGCAATG  
CTACTGTGGTATCTCTGCAGCAGGCCTTGGGCAAGGCCGAGATGCTGTGCTCCACA  
CTGAAAAAGCAGATGAAGTACTTAGAGCAGCAGCAGGATGAGACCAAACAAGCACA  
AGAGGAGGCGGGCCGGCTCAGGAGCAAGATGAAGACCATGGAGCAGATTGAGCTTC  
TACTCCAGAGCCAGCTCCCTGAGGTGGAGGAGATGATCCGAGACATGGGTGTGGGA  
CAGTCAGCGGTGGAACAGCTGGCTGTGTACTGTGTGTCTCTCAAGAAAGAGTACGA  
GAATCTAAAAGAGGCACGGAAGGCCTCAGGGGAGGTGGCTGACAAGCTGAGGAAGG  
ATTTGTTTTTCTCCAGAAGCAAGTTGCAGACAGTCTACTCTGAATTGGATCAGGCC  
AAGTTAGAAGTGAAGTCAGCCCAGAAGGACTTACAGAGTGCTGACAAGGAAATCAT  
GAGCCTGAAAAAGAAGCTAACGATGCTGCAGGAAACCTTGAACCTGCCACCAGTGG  
CCAGTGAGACTGTGCGACCGCCTGGTTTTAGAGAGCCCAGCCCCCTGTGGAGGTGAAT  
CTGAAGCTCCGCCGGCCATCCTTCCGTGATGATATTGATCTCAATGCTACCTTTGA  
TGTGGATACTCCCCCAGCCCCGGCCCTCCAGCTCCCAGCATGGTTACTACGAAAAAC  
TTTGCCTAGAGAAGTCACACTCCCCAATTCAGGATGTCCCCAAGAAGATATGCAAA  
GGCCCCAGGAAGGAGTCCCAGCTCTCACTGGGTGGCCAGAGCTGTGCAGGAGAGCC  
AGATGAGGAAGTGGTTGGTGCCTTCCCTATTTTTGTCCGGAATGCCATCCTAGGCC  
AGAAACAGCCCCAAAAGGCCAGGTCAGAGTCCTCTTGCAGCAAAGATGTGGTAAGG  
ACAGGCTTCGATGGGCTCGGTGGCCGGACAAAATTCATCCAGCCTACTGACACAGT  
CATGATCCGCCCATTGCTGTGTTAAGCCCAAGACCAAGGTTAAGCAGAGGGTGAGGG  
TGAAGACCGTGCTTCTCTCTTCCAGGCCAAGCTGGACACCTTCTGTGGTTCGTGA  
GAACAGTGAGTCTGACCAATGGCCAGACACATGCCTGCAACTGTAGGTCAAGGAC  
TGTCCAGGCAGGGTTTGTGGACAGAGCCCTACTTTCGGGACCAGCCTGAGGTGTAA  
GGGCAGACAAACAGGTGAGGGTGAGTGTGACACCCAGAGACTGCTCTTCTGCCCCT  
CACCTGCCCCACTCCTACGACTGGGAGCTGACATGACCAGCCCACTGATCCTGTC  
AGCAGGTCCTGCTCTGTTGCCAGGCTCTTGTTTATAGCCATGATCAGATGTGGTCA  
GACTCTTTCTGGGCCTGGAGACCACGGTCACTTGTTGACTGTCTCTGTGGACCAGA  
GTGCTTGAGGCATCTCAGGCAGCCTCAGCCCAAGCTTCTACCTGCCTTTGACTTGC  
TTCTAGCATAGCCTGGGCCAAGCAGGGTGGGGAATGGAGGATAGACATGGGATGTA  
TGGAGAGGATGGAAGATTTTCCCGAAAAA

## FIG. 8B

murine TRIP cDNA sequence

GGCACGAGGTGCGGTGGAGCGAAATTTGAAGGAACCGGAGCGGTGGCCGGTTCCAC  
CAAACGTGTGTCTGTCTCTGGCAGCTGGTTCCCTGGGCTGCTTGAGTCGAGCCATCA  
TGCCTATCCTCTCTCTGTGCACTATCTGCTCCGACTTCTTCGATCACTCCCGTGAC  
GTGGCTGCCATCCACTGTGGCCACACTTTTCATCTGCAATGCCTAATCCAGTG GTT  
TGAGACAGCACCAAGTCGGACCTGCCACAGTGTAGAATCCAGGTTGGCAAAAAGA  
CTATTATAAACAAACTTTTCTTTGACCTCGCCCAGGAAGAGGAGAATGTCTTGAT  
GCAGAATTCTTAAAGAATGAACTGGACAGCGTCAAAGCTCAGCTTTCCCAGAAAGA  
CAGGGAGAAACGGGACAGCCAGGCCATTATCGACACTCTACGGGACACCCTGGAAG  
AACGCAATGCTACCGTGGAGTCCCTACAGAACGCCTTAAACAAGGCAGAGATGCTG  
TGTTCCACCCTGAAAAACAGATGAAGTTCCTGGAGCAGCGGCAGGATGAGACCAA  
ACAAGCTCGGGAGGAGGCCACCGACTCAAGTGCAAGATGAAAACCATGGAGCAAA  
TTGAGCTCCTACTCCAGAGCCAGCGTTCTGAGGTGGAGGAGATGATTTCGAGACATG  
GGTGTGGGACAGTCAGCGGTGGAGCAGCTGGCTGTGTACTGCGTGTCCCTCAAGAA  
AGAGTATGAGAATCTGAAGGAAGCTCGGAAGGCCACAGGGGAACTGGCTGACAGGT  
TGAAGAAGGATTTGGTGTCTCTAGGAGCAAGTTGAAGACTCTCAACACTGAGCTG  
GATCAGGCCAAGTTAGAACTGAGGTGAGCCAGAAAGGACTTACAAAGTGCTGACCA  
GGAGATCACGAGCCTAAGAAAGAAGCTGATGATCCTCCAGGGAACCTTGAGCCTGC  
CTCCGCGTACCAATGAGACGGTCAGCCGCCTGGTTTTTTGAGAGCCCAGCCCCTGTG  
GAGATGATGAACCCGAGGCTTCACCAGCCACCCTTCGGTGATGAGATTGATCTCAA  
TACCACCTTTGATGTAAATACCCCTCCAACCCAGACCTCTGGCTCCCAGCATTGCC  
TCCCCAAGAAGCTGTGCCTGGAGAGGGCAGCTCTCCCATGCAGAATGTCCTCAAG  
AAGGTGCACAAAGTCTCCAAGCCGGAGTCCCAGCTCTCACTGGGTGGCCAGCGATG  
TGTAGGAGAGCTAGATGAGGAACTGGCTGGTGCCTTCCCTCTCTTCATCCGGAATG  
CTGTCCTGGGTGAGAAACAGCCCAACAGGACCACAGCAGAATCCCGAAGCAGCACA  
GATGTGGTAAGAATAGGCTTTGATGGGCTTGAGGACGAACAAAATTCATCCAGCC  
TAGGGACACAACCATTATCCGACCAGTGCCCTGTTAAGTCCAAGGCCAAGAGTAAAC  
AGAAAGTGAGAATAAAGACTGTGAGTTCTGCCTCCCAGCCCAAGCTGGATACCTTC  
TTATGTCAGTGAACGGTGACCAGAGTGATGTTTGCAATTAGTGGGCCAAGACCTGG  
CTAACCGGAAGTGTTTTTTGGAAGATGGCTCCTCTTGGAACAGTCCAAGAGAGATGC  
CCAGAAAACACACTTCCTGTGTTCACTGCGCCCTGCACCACACTGGGAAGCCACAT  
GACCAGTTTACTGTTCCGATCAGCAGGGCCTACTTCCAGTTGCAGGGTTTTTGCTTA  
TAGCTACAACCAGGTGTGGCTGGACTCCTTTTGTTTTTTATAGAACAGGGTCACATT  
GACTCTAAGTGGATGGGAGTGCTGGAGGATCCTATGCAGGCTGGAGGACCCTGCGC  
TTGAACTCCTGCCTGCCTCCAGCTTATTGCTTGAAATTATGGGGTGAGGTGGTGAT  
AGGGAAAGGTTGGGGAAGTTTTCTGTGTAAATAAAAAGGGATCTTTTCTTCAAAA  
AAAAAAAAAAAAAAAA